

L. Helms

Re-run



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,840B

DATE: 04/04/2002
TIME: 11:40:23

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Output Set: N:\CRF3\04032002\I424840B.raw

3 <110> APPLICANT: Berchtold, Peter
4 Escher, Robert F. A.
6 <120> TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
8 <130> FILE REFERENCE: 100564-09049
10 <140> CURRENT APPLICATION NUMBER: 09/424,840B
11 <141> CURRENT FILING DATE: 1999-12-03
13 <150> PRIOR APPLICATION NUMBER: DE 19820663.1
14 <151> PRIOR FILING DATE: 1998-05-08
16 <150> PRIOR APPLICATION NUMBER: DE 19755227.7
17 <151> PRIOR FILING DATE: 1997-12-12
19 <150> PRIOR APPLICATION NUMBER: DE 19723904.8
20 <151> PRIOR FILING DATE: 1997-06-06
22 <160> NUMBER OF SEQ ID NOS: 128
24 <170> SOFTWARE: PatentIn version 3.1
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28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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40 1 5 10 15 96
42 acc ctg tcc ctc aac tgc act gtc tct ggt cgc tcc atc agt ggt tac
43 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr 30
44 20 25 30 144
46 tct tgg aga tgg atc cgg cag tct cca ggg aag gga cta gag tgg att
47 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile 45
48 35 40 45 192
50 ggg gat atc tct tat agt ggg agt acc aag tac aaa ccc tcc ctc agg
51 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg 60
52 50 55 60 240
54 agt cga gtc acc ctg tca gta gac acg tcc aag aac cag ttc tcc ctg
55 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu 75 80
56 65 70 75 288
58 aag ctg aat tcg gtg acc gct gcg gac acg gcc gtc tat tac tgt gcg
59 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala 95
60 85 90 336
62 cga gtc ttg ccc ttt gac ccg atc tcg atg gac gtc tgg ggc aaa ggg
63 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly

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86 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
87          35          40          45
90 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
91          50          55          60
94 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
95 65          70          75          80
98 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
99          85          90          95
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126 acc atc tct tgt tct ggg agc agc tcc aac atc aga agt aat cct gtt          96
127 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
128          20          25          30
130 agc tgg tat cac cag gtc cca ggc acg gcc ccc aaa ctc ctc atc ttt          144
131 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
132          35          40          45
134 ggt agt cat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc          192
135 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
136          50          55          60
138 aag tcg ggc acc tcc gcc tcc ctg gcc atc cgt ggg ctc caa tct ggg          240
139 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
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143 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
144      85      90      95
146 ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc      333
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152 <211> LENGTH: 111
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166 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
167      35      40      45
170 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
171      50      55      60
174 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
175 65      70      75      80
178 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
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182 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
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203 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
204      20      25      30
206 gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg      144
207 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
208      35      40      45
210 gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac tcc gtg      192
211 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
212      50      55      60
214 aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac acg ctg tat      240
215 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
216 65      70      75      80

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218 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt      288
219 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
220                               85                               90                               95
222 gcg aga gcg ctg ggg agc tgg ggg ggt tgg gac cac tac atg gac gtc      336
223 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
224                               100                               105                               110
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227 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
228                               115                               120
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232 <211> LENGTH: 123
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242 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
243                               20                               25                               30
246 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
247                               35                               40                               45
250 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
251                               50                               55                               60
254 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
255 65                               70                               75                               80
258 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
259                               85                               90                               95
262 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
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284 1                               5                               10                               15
286 acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat act gta      96
287 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
288                               20                               25                               30
290 aac tgg tac cag cag ctc cca gga acg gcc ccc aaa ctc ctc atc tat      144
291 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
292                               35                               40                               45
294 agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc      192

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295 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
296      50      55      60
298 aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag      240
299 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
300 65      70      75      80
302 gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg aat ggt      288
303 Asp Glu Ala Asp Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
304      85      90      95
306 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc      333
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312 <211> LENGTH: 111
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326 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
327      35      40      45
330 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
331      50      55      60
334 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
335 65      70      75      80
338 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
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349 <213> ORGANISM: Homo sapiens
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353 <222> LOCATION: (1)..(369)
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362 tcc ctg aga ctc tct tgt gca gcc tct gga ttt acg ttt gac aac ttt      96
363 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
364      20      25      30
366 gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc      144
367 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
368      35      40      45
370 tca ggc att agt ggt ggt ggt ctt ttg aca cac tac gca gac tcc gtg      192

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VERIFICATION SUMMARY

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